Molecular Genetic Tools for Assessing the Status and Vulnerability of Aquatic Resources

Evon Hekkala
Postdoctoral Scientist
U.S. EPA Office of Research and Development (ORD)/National Exposure Research Laboratory (NERL)/Ecological Exposure Research Division (EERD)
(513) 569-7416
hekkala.evon@epa.gov

Authors: Mark Bagley, Michael Blum, Susan Franson, Evon Hekkala, Suzanne Jackson, Eric Waits
U.S. EPA ORD/NERL/EERD

Development of ecological indicators that efficiently capture the present condition and project future vulnerabilities of biological resources is critical to sound environmental management. For this reason, the ORD's Ecological Research Program is developing genetic methodologies to supplement and improve existing ecological indicators for aquatic ecosystems. Five research areas that can potentially improve the science of ecological assessment through incorporation of genetic methods are under active investigation: (1) development of accurate and precise methods for biological identification of aquatic species and subspecies, (2) delineation of ecological assessment units through analysis of genetic structure across multiple species, (3) assessment of changes in genetic diversity as an indicator of present and historical environmental condition, (4) assessment of genetic diversity at diagnostic loci and across the genome as an indicator of vulnerability to future environmental perturbations, and (5) integrated assessments to link landscape-level stressors to population-level outcomes. A number of these research applications were recently explored in the Mid-Atlantic Integrated Assessment (MAIA) area. Molecular genetic analysis documented that species identification based on morphological analysis in the field was reasonably accurate. However, for two of three fish species assessed across the MAIA region, genetic analysis revealed highly distinct groups that likely represent undescribed species or subspecies. Geographic correspondence of genetic structure across these species suggested that genetics could be used to refine biogeographic boundaries. Each of the fish species displayed characteristic associations between genetic diversity and various environmental parameters. Ongoing work on invasive species utilizes "DNA taxonomy" for identifying morphologically indistinct organisms in ballast water and recipient waters as well as for documenting rates of introgressive hybridization between invading and resident stream fish. Ongoing collaborative research in landscape ecology, genetics, and population modeling is aimed at addressing questions of resource vulnerability and design of integrated ecological assessments. Ultimately, this work will produce highly effective tools that the states, tribes, and U.S. Environmental Protection Agency (U.S. EPA) regions will be able to implement for assessing and protecting the aquatic biodiversity.